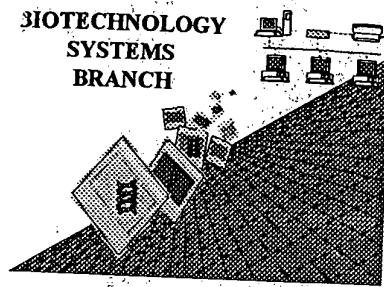


Yul
Mailed on or about 9/27/99

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/009 802A

Art Unit / Team No.: 1636

Date Processed by STIC: 9/13/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/009,802A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is Intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

3 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1636

PAGE: 1

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999

TIME: 12:48:44

Input Set: I009802A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Set PP.512

1 <110> APPLICANT: McCarthy, Sean A.
2 <120> TITLE OF INVENTION: NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
3 THEREFOR
4 <130> FILE REFERENCE: MEI-008
5 <140> CURRENT APPLICATION NUMBER: US/09/009,802A
6 <141> CURRENT FILING DATE: 1998-01-20
7 <150> EARLIER APPLICATION NUMBER: 08/842,898
8 <151> EARLIER FILING DATE: 1997-04-17
9 <150> EARLIER APPLICATION NUMBER: 60/071,589
10 <151> EARLIER FILING DATE: 1998-01-15
11 <160> NUMBER OF SEQ ID NOS: 19
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 2479
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (38)..(1087)
20 <400> SEQUENCE: 1
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23 1 5
24 acc ctg ctg tgc ctg ctg gcg gcg gcg gtc ccc acg gcc ccc gcg 103
25 Thr Leu Leu Cys Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
26 10 15 20
27 ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
28 Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
29 25 30 35
30 agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199
31 Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
32 40 45 50
33 gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247
34 Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
35 55 60 65 70
36 gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac 295
37 Glu Met Glu Ala Glu Ala Ala Lys Ala Ser Ser Glu Val Asn
38 75 80 85
39 ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg 343
40 Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
41 90 95 100
42 aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata 391
43 Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile
44 105 110 115

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802ADATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

45	acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
46	Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
47	120 125 130	
48	tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
49	Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
50	135 140 145 150	
51	gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac	535
52	Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
53	155 160 165	
54	acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt	583
55	Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
56	170 175 180	
57	gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg	631
58	Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
59	185 190 195	
60	gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc	679
61	Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
62	200 205 210	
63	cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg	727
64	Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
65	215 220 225 230	
66	tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc	775
67	Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
68	235 240 245	
69	cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
70	Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
71	250 255 260	
72	gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
73	Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
74	265 270 275	
75	agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa	919
76	Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
77	280 285 290	
78	gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt	967
79	Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val	
80	295 300 305 310	
81	ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg	1015
82	Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg	
83	315 320 325	
84	agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct	1063
85	Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala	
86	330 335 340	
87	gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggttagatgtg	1117
88	Ala Leu Leu Gly Arg Glu Glu Ile	
89	345 350 see item 10 on Error Summary Sheet	
W--> 90	caatagaaat agctaattta tttcccccang tttgtgtcttt aagcgtggc tgaccaggct	1177
91	tcttcctaca tcttcctccc agtaagttc ccctctggct tgacagcatg aggtgttgtg	1237
92	catttgttca gctcccccaag gctgttctcc aggcttcaca gtctggct tgggagagtc	1297
93	aggcagggtt aaaactgcagg agcaggttgc caccctgtc cagattattg gctgcttgc	1357
94	ctctaccagt tggcagacag ccgttgttc tacatggctt tgataattgt ttgagggag	1417

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802ADATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

145	210	215	220	
146	Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu			
147	225	230	235	240
148	Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu			
149	245	250	255	
150	Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu			
151	260	265	270	
152	Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe			
153	275	280	285	
154	Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val			
155	290	295	300	
156	Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu			
157	305	310	315	320
158	Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu			
159	325	330	335	
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161	340	345	350	
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163	<211> LENGTH: 1050			
164	<212> TYPE: DNA			
165	<213> ORGANISM: Homo sapiens			
166	<220> FEATURE:			
167	<221> NAME/KEY: CDS			
168	<222> LOCATION: (1)..(1050)			
169	<400> SEQUENCE: 3			
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171	Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Ala Ala Ala			
172	1 5 10 15			
173	gtc ccc acg gcc ccc gtc ccc gct ccg acg gtc acc tcg gtc cca gtc	96		
174	Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val			
175	20 25 30			
176	aag ccc ggc ccg gtc ctc agc tac ccg cag gag gag gcc acc ctc aat	144		
177	Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn			
178	35 40 45			
179	gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa	192		
180	Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys			
181	50 55 60			
182	ttg cgc agc gtc gtg gaa gag atg gag gca gaa gaa gtc gtc gtc aaa	240		
183	Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys			
184	65 70 75 80			
185	gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat	288		
186	Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn			
187	85 90 95			
188	gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac	336		
189	Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His			
190	100 105 110			
191	cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt	384		
192	Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe			
193	115 120 125			
194	tca gag aca gtt atc aca tct gtg gga gac gaa ggc aga agg agc	432		

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802ADATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

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195      Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
196          130          135          140
197      cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag      480
198      His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
199          145          150          155          160
200      ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg      528
201      Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
202          165          170          175
203      ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg      576
204      Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
205          180          185          190
206      ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt      624
207      Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
208          195          200          205
209      gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga      672
210      Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
211          210          215          220
212      ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt      720
213      Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
214          225          230          235          240
215      tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta      768
216      Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
217          245          250          255
218      gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc      816
219      Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
220          260          265          270
221      tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc      864
222      Cys Gln Pro His Ser His Leu Val Tyr Val Cys Lys Pro Thr Phe
223          275          280          285
224      gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc      912
225      Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
226          290          295          300
227      ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag      960
228      Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
229          305          310          315          320
230      ctg gag gac ctg gag agg agc ctg act gaa gag atg ggc ctg agg gag      1008
231      Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
232          325          330          335
233      cct gcg gct gcc gcc gct gca ctg ctg gga agg gaa gag att          1050
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235          340          345          350
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237      <211> LENGTH: 848
238      <212> TYPE: DNA
239      <213> ORGANISM: Homo sapiens
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243      <400> SEQUENCE: 4
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

FYI

VERIFICATION SUMMARY
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

Line ? Error/Warning

90 W "N" or "Xaa" used: Feature required
442 W "N" or "Xaa" used: Feature required
587 W Invalid/Missing Amino Acid Numbering

Original Text

caatagaaat agctaattta tttccccang tgtgtgct
accccattn attctagagt cnagaacgca aggatctc